

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (original) A method of determining whether to use a RB2/p130 gene expression system or a protein encoded by the system to modulate a gene or gene expression pattern in lung cancer cells of a human test subject, the method comprising:

providing molecular signatures modulated by RB2/p130 for lung cancer cells, wherein the molecular signatures comprise expression products of at least one of the genes selected from the group consisting of: PCNA, MKK3, B-MYB, CCNF, BUB1B, PLK, NIK, KNSL2, PCSK7, CCNB2, GPRK6, HCFC1, PFAS, DNMT1, KPNA2, STK15, TIEG, BUB1 ELK1, UMPK, PMI, CAMKK2, GSK3B, HADHSC, POLD1, NOL1, EMK1, GRP-R, XRCC3, CHK, MAGEA3/6, PPM1G, TRAF5, ABCF2, TEAD4, PIM1, CCND1, CDR2, PSMB2 and RAF1; determining gene or genes expressed in the lung cancer cells of the human test subject; and

using the RB2/p130 gene expression system or the protein to modulate the gene or the gene expression pattern in the lung cancer cells of the human test subject if it is determined that the gene or genes expressed in the lung cancer cells of the human test subject are the same as the at least one of the genes.

2. (original) The method of claim 1 wherein the genes selected are B-MYB, PCSK7, STK15, ELK1, NOL1, MAGEA3/6, PIM1, CCND1, CDR2, and RAF1.

3. (original) The method of claim 1, wherein the human test subject is post-treatment for a non-small cell lung cancer.

4. (original) The method of claim 3, wherein the treatment is selected from the

group consisting of surgical operation, chemotherapy, radiation therapy and RB2/p130 gene therapy or combinations thereof.

5. (new) A method of identifying a patient suspected of having non-small cell lung cancer comprising

obtaining a cell or tissue sample of the patient;

exogenously expressing RB2/p130 gene in said sample;

assaying for expression of a gene set in said cell or tissue sample, wherein down-regulation of transcription of the gene set in said sample is indicative of possible presence of lung cancer.

6. (new) The method of claim 5, wherein the gene set is PCNA, MKK3, B-MYB, and NIK.

7. (new) The method of claim 5, wherein the gene set is RAF-1, PIM1, CycD1, GRPR, KPNA2, and CycB2.

8. (new) The method of claim 5, wherein the gene set is B-MYB, PCSK7, STK15, ELK1, NOL1, MAGEA3/6, PIM1, CCND1, CDR2, and RAF1

9. (new) The method of claim 5, wherein the gene set is CCNF, BUB1B,PLK, , KNSL2, PCSK7, CCNB2, GPRK6, HCFC1, PFAS, DNMT1, STK15, TIEG, BUB1 ELK1, UMPK, PMI, CAMKK2, GSK3B, HADHSC, POLD1, NOL1, EMK1, XRCC3, CHK, MAGEA3/6, PPM1G, TRAF5, ABCF2, TEAD4, CCND1, CDR2 and PSMB2.

10. (new) The method of claim 5, wherein the gene set is PCNA, MKK3, B-MYB, CCNF, BUB1B,PLK, NIK, KNSL2, PCSK7, CCNB2, GPRK6, HCFC1, PFAS, DNMT1, KPNA2, STK15, TIEG, BUB1 ELK1, UMPK, PMI, CAMKK2, GSK3B, HADHSC, POLD1,

NOL1, EMK1, GRP-R, XRCC3, CHK, MAGEA3/6, PPM1G, TRAF5, ABCF2, TEAD4, PIM1, CCND1, CDR2, PSMB2 and RAF1.

11. (new) The method of claim 5, wherein the step of assaying involves the use of an oligonucleotide microarray assay.

12. (new) The method of claim 5, wherein the patient is post-treatment for a non-small cell lung cancer.

13. (new) A method of diagnosing non-small cell lung cancer in a patient comprising assaying a cell or tissue sample of the patient after exogenously expressing RB2/p130 gene in said sample; and

determining whether there is down-regulation of transcription of at least one of PCNA, MKK3, B-MYB, and NIK genes, wherein the down-regulation is indicative of said lung cancer.

14. (new) The method of claim 13, wherein, in the step of determining, down-regulation of transcription of at least one of RAF-1, PIM1, CycD1, GRPR, KPNA2, and CycB2 genes is determined.

15. (new) The method of claim 13, wherein the gene set is B-MYB, PCSK7, STK15, ELK1, NOL1, MAGEA3/6, PIM1, CCND1, CDR2, and RAF1.

16. (new) The method of claim 13, wherein, in the step of determining, down-regulation of transcription of at least one of CCNF, BUB1B, PLK, , KNSL2, PCSK7, CCNB2, GPRK6, HCFC1, PFAS, DNMT1, STK15, TIEG, BUB1 ELK1, UMPK, PMI, CAMKK2, GSK3B, HADHSC, POLD1, NOL1, EMK1, XRCC3, CHK, MAGEA3/6, PPM1G, TRAF5, ABCF2, TEAD4, CCND1, CDR2 and PSMB2 genes is determined.

17. (new) The method of claim 13, wherein, in the step of determining, down-regulation of transcription of PCNA, MKK3, B-MYB, CCNF, BUB1B, PLK, NIK, KNSL2, PCSK7, CCNB2, GPRK6, HCFC1, PFAS, DNMT1, KPNA2, STK15, TIEG, BUB1 ELK1, UMPK, PMI, CAMKK2, GSK3B, HADHSC, POLD1, NOL1, EMK1, GRP-R, XRCC3, CHK, MAGEA3/6, PPM1G, TRAF5, ABCF2, TEAD4, PIM1, CCND1, CDR2, PSMB2 and RAF1 genes is determined.

18. (new) The method of claim 13, wherein the patient is post-treatment for a non-small cell lung cancer.

19. (new) The method of claim 13, wherein, in the step of determining, down-regulation of protein expression of MKK3, B-MYB, and NIK is determined instead of transcriptional down-regulation of said genes

20. (new) The method of claim 13, further comprising determining down-regulation of protein expression of at least one of B-MYB, MAGEA3/6, MKK3, NIK, PCNA, PLK and RAF1 is determined.